

09/673,222 IDS Ref #50



CGCTCAGGATACGACTTCGCTAGATCGGATCCCGGATATTATATAGCTCGATCGATC
TTCTCTATATCCGCGATGGGATATATACACACACACCGCGGATAGCATGACTGATCT
CCCCATCT
CACAGACTCTACGCT

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	MIM	Books
Search		Nucleotide	for			Go	Clear	
Limits		Preview/Index		History		Clipboard		Details
Display	default	Save	Text	Add to Clipboard		Get Subsequence		

☐ 1: X66400. *S.cerevisiae* SUG1...[gi:4590]

Links

LOCUS SCSUG1 1671 bp DNA linear PLN 17-AUG-1994
DEFINITION *S.cerevisiae* SUG1 gene.
ACCESSION X66400
VERSION X66400.1 GI:4590
KEYWORDS ATPase; sug1 gene.
SOURCE *Saccharomyces cerevisiae* (baker's yeast)
ORGANISM *Saccharomyces cerevisiae*
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 1671)
AUTHORS Swaffield, J.C., Bromberg, J.F. and Johnston, S.A.
TITLE Alterations in a yeast protein resembling HIV Tat-binding protein
relieve requirement for an acidic activation domain in GAL4
JOURNAL Nature 357 (6380), 698-700 (1992)
MEDLINE 92310548
REFERENCE 2 (bases 1 to 1671)
AUTHORS Wolfe, K.H.
TITLE Similarity between putative ATP-binding sites in land plant plastid
ORF2280 proteins and the FtsH/CDC48 family of ATPases
JOURNAL Curr. Genet. 25 (4), 379-383 (1994)
MEDLINE 94363756
REFERENCE 3 (bases 1 to 1671)
AUTHORS Johnston, S.A.
TITLE Direct Submission
JOURNAL Submitted (21-MAY-1992) S.A. Johnston, Ut Southwestern Medical
Center, 5323 Harry Hines Blvd, Dallas Tx 75235 8573, USA
FEATURES
source 1..1671
/organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
/chromosome="VII"
gene 336..1553
/gene="sug1"
CDS 336..1553
/gene="sug1"
/codon_start=1
/protein_id="CAA47023.1"
/db_xref="GI:4591"
/db_xref="SWISS-PROT:Q01939"
/translation="MTAAVTSSNIVLETHESGIKPYFEQKIQETELKIRSKTENGRRRL
EAQRNALNDKVRFIKDELRLQLQEPGSYVGEVIKIVSDKKVLVKVQPEGKYIVDVAKDI
NVKDLKASQVRVCLRSDSYMLHKVLENKADPLVSLMMVEKVPDSTYDMVGGLTKQIKEI
KEVIELPVKHPFELFESLGIAQPKGVILYGPPTGKTLARAVAHHTDCKFIRVSGAEL
VQKYIGESRMVRELFVMAREHAPSIIIFMDEIDSIGSTRVEGSGGGDSEVQRTMLELL
NQLDGFETSKNIKIIMATNRLDILDPALLRPGRIDRKIEFPPPSVAARAEILRIHSRK
MNLTRGINLRKVAEKMNGCSGADVKGVCTEAGMYALRRERRIHVTQEDFELAVGKVMNK
NQETAISVAKLFLK"
misc feature 894..941
/gene="sug1"
/product="ATPase"
BASE COUNT 529 a 289 c 366 g 487 t

ORIGIN

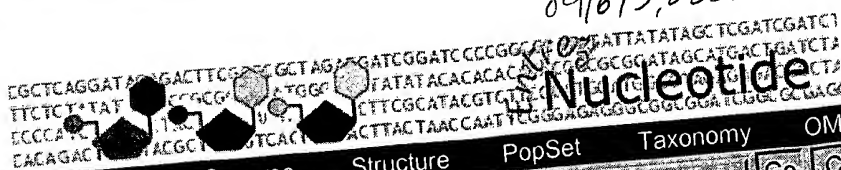
```
1  gaattcgctt  tggaaatggc  accgttgccc  cacacgtaac  aaaaagagcc  ttttcttcaa
61  taatacccat  tgtttgaaag  agctggcttc  tgactcgttt  gtttaacctc  tttttgcgac
121  tgaaaacttg  tttttctatt  tccctttttc  ttcgggtggg  ttttttaata  tgaaatcata
181  ttttgcatac  ttctctaccc  ttattcttgt  tcggaaattt  tcgtatttta  aaactgtcaa
241  aatgcgagcg  aggtggcaaa  agttgtaata  tcagtaacag  ttaggttagg  ttttatgtaa
301  acggaacaac  agtatagtgg  gatactatca  cgacaatgac  agctgctgta  acatcctcca
361  atatagtatt  agaaaccac  gaaagtggta  tcaaaccata  ttttgaacag  aagatccaag
421  aaacagaatt  aaagatccgc  tccaaaacag  aaaatggtcg  cagactggaa  gctcaaagga
481  atgcattgaa  tgacaaagta  cgttttatca  aggacgaact  gcgtctatta  caggaacctg
541  gatcttatgt  ggggtgaagt  ataaagatcg  tgtctgacaa  aaaagtcttc  gttaaagtgc
601  aacctgaggg  aaaatacatc  gtggatgttg  caaaagatat  aaacgtgaag  gacttaaagg
661  catctcaaag  agtttgtcta  aggagtgact  cttatatgtt  gcataaagtt  cttgagaata
721  aggetgaccc  actagtttcg  ttgatgatgg  tggaaaaagt  tcctgattcc  acatacgata
781  tggttggtgg  tttgacaaag  caaataaagg  agattaaaga  agttattgaa  ttgcccgtaa
841  aacatcctga  actttttgaa  agtttgggta  ttgcgcaacc  aaagggtgtc  atcttatatg
901  gcccccttg  tacagggaaa  accttattgg  caagagctgt  cgcacatcac  actgattgta
961  aattcatcag  ggtcagtgg  gcggaactgg  tacaaaagta  tatcggcgaa  gggtcccgtg
1021  tggtcctgta  gctgttttg  atggctagag  aacatgctcc  ctcaattatc  tttatggatg
1081  aaatcgattc  cattggctct  actcgtgtag  aaggttctgg  tgggtggtgat  tcagaagttc
1141  aaagaacaat  gttagaacta  ctaaaccaat  tggacgggtt  tgaaacttct  aaaaatatca
1201  agatcataat  ggccacgaat  agactagata  ttctagatcc  agcacttttg  agaccggta
1261  gaatagatag  gaagattgaa  tttccacctc  caagtgtcgc  agctagagct  gaaattttaa
1321  gaatccattc  cagaaaaatg  aatctaactc  gtggtatcaa  cttgagaaaag  gttgctgaaa
1381  agatgaacgg  ttgttctgg  gccgatgtca  aagggtgtctg  tacagaagct  ggtatgtatg
1441  ctttaagaga  aagaagaata  cacgttactc  aagaagactt  cgaactcgct  gtgggtaagg
1501  ttatgaacaa  gaaccaagaa  acggccattt  ctgtcgccaa  gctgttcaag  tgatgtattc
1561  gtttcacttg  gctcattgta  tatgttactt  agtgtatgtg  tataatatca  tagtttagca
1621  ttaactaaga  ggcaaaatta  taccgctgga  tatacaggat  ataacggtac  c
```

//

Revised: July 5, 2002.

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLN](#) | [NIH](#)

Oct 31 2002 16:00:17



NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM Book

Search Nucleotide for

Limits Preview/Index History Clipboard Details

Display default Save Text Add to Clipboard Get Subsequence

Links

1: L25423. *Caenorhabditis* el...[gi:409130]

☒ 1: L25423. *Caenorhabditis el...*[gi:409130]
 LOCUS CELMEI1SP 3267 bp DNA linear INV 03-MAR-1994
Caenorhabditis elegans mei-1 gene exons 1-4, complete cds.

LOCUS	CELMEI1SP
DEFINITION	Caenorhabditis elegans mei-1 gene exons 1-4, complete
ACCESSION	L25423
VERSION	L25423.1 GI:409130
KEYWORDS	ATPase.
SOURCE	Caenorhabditis elegans
ORGANISM	<u>Caenorhabditis elegans</u> Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE	1 (bases 1 to 3267)
AUTHORS	Clark-Maguire, S. and Mains, P.E.
TITLE	mei-1, a gene required for meiotic spindle formation in Caenorhabditis elegans, is a member of a family of ATPases
JOURNAL	Genetics 136 (2), 533-546 (1994)
MEDLINE	94200595
PUBMED	8150281
COMMENT	Original source text: Caenorhabditis elegans (strain Bristol) mixed DNA.

```

COMMENT      Original  

             mixed DNA.
FEATURES             Location/Qualifiers
     source             1..3267
                        /organism="Caenorhabditis elegans"
                        /strain="Bristol N2"
                        /db_xref="taxon:6239"
                        /dev_stage="mixed"
                        /germline
     misc_binding      233..240
                        /gene="mei-1"
                        /bound_moiety="ATP"
     misc_binding      288..292
                        /gene="mei-1"
                        /bound_moiety="ATP"
     exon              910..1087
                        /gene="mei-1"
                        /number=1
     gene              join(911..1087,1138..1476,1523..2250,2576..2750)
                        /gene="mei-1"
                        join(911..1087,1138..1476,1523..2250,2576..2750)
     CDS              /gene="mei-1"
                        /function="meiotic spindle formation"
                        /codon_start=1
                        /protein_id="AAA28109.1"
                        /db_xref="GI:409131"
                        /translation="MNGDVQSVIRGYLERAQVAKTMSDAGRWNEAGDLLRQLMTDVKS
CKISASNRDEHDARNTFLRALEANLKL VQQNV RDEDDLHEAMTRQSGSPEPPADPDVW
SKPSPPLPSSSKFGATKKG VGAAGPRPREISKSTSSMSTNPADV KPANPTQGILPQNS
AGDSFDASAYDAYIVQAVRGTMATNTENTMSLDDIIGMHDVKQVLHEAVTLPLLVP EF
FQGLRSPWKAMVLAGPPGTGKTLIARAIASESSSTFTVSSD LSSKWRGDSEKIVRL
LFELARFYAPSIIFIDEIDTLGGQRGNSGEHEASRRVKSEFLVQMDG SQNKFD SRRVF
VLAATNIPWELDEALRRRFEKRIFIP LPDIDARKK LIEKSMEGTPKSD EINYDDL AAR
TEGFSGADV VSLCRTAAINVLR RYDTKSLRG GELTAAMESLKAELVRNIDFEALQAV
SPSAGPDTMLKCKEWCDSFGAM"

```

intron 1088..1137
/gene="mei-1"
/number=1
exon 1138..1476
/gene="mei-1"
/number=2
intron 1477..1522
/gene="mei-1"
/number=2
exon 1523..2250
/gene="mei-1"
/number=3
intron 2251..2575
/gene="mei-1"
/note="alternate splice site"
/number=3
intron 2251..2566
/gene="mei-1"
/number=3
exon 2567..2942
/gene="mei-1"
/number=4
exon 2576..2942
/number=4
polyA site 2942
/gene="mei-1"

BASE COUNT 1029 a 612 c 641 g 985 t
ORIGIN

```

1 gaattccgct aaaattcgaa aattgaaagt gttcaaattg caagcgattg tgcatacagac
61 gtgacagtgt ctgggggtgta ttgcgtccga cattttaact gacgacactt gtacttttcg
121 catactccgg agctccagct ccgcggagcc ctgagcaatt atttttttac tttttatgaa
181 aagcttctat agatatcttt taagaagtta cactataatt gtgcaaataa aactgggtcc
241 ggacaacaca aatttcgtct atacctttat gatctttttt ttgttaaaca agtgaaacaa
301 ttatttcctt ttcaaactgc tcttgtttct tctctttatt aatcaatttt ttttttttg
361 ctttgtgtaa aggaattgtt tgtcgcggat gagctaattc tgaggtttga ccagcagaaa
421 tctgttttct gaaaaatcaa taactcgccg ctttaatttg gttttattca agtgatatgc
481 aattagaagg ttctaatacat ttatatctcg ctgaaagatc tcagatttca agccttttgc
541 taaggattta attcctaataa ctttttttga cctatcattt tttgtgtgat ctaccgctgt
601 aaataactgt tgttttgcgg ctaaactctt tcaatgtttc caacaagtga gccaatatca
661 agtaaaaaaa gaaaaatcgt tttctattca accattttat tctgtaaata atattaaatt
721 catcttcacg gtacaatctt cttctcccat ctaataaagt ccacgcacac tccgttccgt
781 cgtttcccta ttcgttatca ttcatcatct tgccattttc ttctccgcca aatcccattg
841 tcttatacta aatttcattc tctcgtctgt agaagtgtat attattgaaa aattaaagta
901 tattttcagg atgaatgggg atgtgcagtc agtcattcgc ggatatctgg agcgagccca
961 agtcgcgaaa acaatgtccg atgccggacg atggaatgag gctggtgatc ttcttcgtca
1021 gtcatacaga gatgtcaaaa gctgtaaaat ttcggcaagc aacagagacg agcatgacgc
1081 aagaaatgta cgtaataata atcttttaaa agcttggtga attatttgaa atttcagaca
1141 ttcctacagc ccctagaggc taatttgaag cttgtccaac aaaaatgtgc cgatgaagat
1201 gacctacacg aggcgatgac gcgacaaaagt ggaagtccag agccacctgc agaccagat
1261 gtttgggtcca aaccatcgcc accgttacca tcctcatcga aatttggagc aacaaagaaa
1321 ggagttggag cagcaggtcc acgtcccaga gaaatatcaa agtcaacgtc gtcgatgagc
1381 acgaatccgg ctgatgtgaa gcctgcgaat ccaacacaag gaatactgcc tcaaaatagt
1441 gctggagatt cattcgatgc atcggcttat gatgcggtaa gttattatgt tttccagaaa
1501 caaaaatcag aaatcttttc agtacattgt tcaagcgggt cggtgtacaa tgggtacaaa
1561 tacggaaaat acaatgtctt tagatgatat aatcggaatg cacgacgtga agcaagttct
1621 gcacgaagcc gtcactcttc cactcttggt gccagaattc ttccagggtc tccgttcacc
1681 atggaaaagca atggttctcg ctggaccacc tggaactgga aagactctta tcgcacgtgc
1741 gattgcttca gagtctagtt caactttttt taccgtttcc tcgactgatc tgtccagcaa
1801 gtggcgtggt gattccgaga agattgttgc tctgttattc gaacttgcac gggtctatgc
1861 tccatccata atcttcatcg atgagattga cacacttggt ggacaacgtg gaaattctgg
1921 agaacacgaa gcgagtcggc gtgttaaata cgagtttctg gtacaaatgg acgggtcaca
1981 gaataaattc gattcgcgac gtgtattcgt gctggccgcc acaaatattc catgggagct
2041 cgatgaggca ctccgaagac gtttcgaaaa gcgaatcttc attccactgc cagatataga
2101 tgcaagaaag aagcttatcg aaaaatcaat ggaaggaact ccgaaatccg atgaaattaa
2161 ctatgatgac ttggcggcaa ggactgaagg attctcagga gctgatgttg tgtctctatg

```

```

2221 cagaactgct gctatcaatg tgttgagaag gtaggtagca ggaatgtgca gaaaatcttt
2281 ttggaaaacg tgcttggttc aataagataa tccaatattt cgaatcaaaa ctggatatag
2341 aatggcaact ttcattgact atttaattgt tttaacgctt gtagacaaat taaataacat
2401 ttttaagatga aatgaaccgt ttttataaat ttcgatatca atttaagatt gaaaagtgtg
2461 attatcataa ttaaaaaaaaa gccaattttg tacgtttgct gaaaaaatat tgctaatacg
2521 gatgttgcaa cacttttttc aagaatcgac actaagaatc ctttaagatat ttcagatagc
2581 acaccaaatac attgcgaggc ggggaactga cagctgcaat ggaatcactg aaagccgaac
2641 tcgtgaggaa cattgacttt gaagcagctc ttcaagcagt ttcaccaagt gctgggtccag
2701 atacaatgct caaatgcaaa gaatggtgtg actcttttgg tgccatgtaa atcaactatt
2761 tattgtgatc tccttttagt ttaaaatatt gtggcctagc tttgggtttt gaaactctga
2821 aacattgtac agataaaatt ttcaaggcca ccttcattcca aacatctctc cccgattcac
2881 tctttctctg taaataactta ttggttaaat ttgtatgtaa aatgaatcat tttgccactc
2941 actggattat ttggaaatat ataaaagtgc atttgtgaaa gaaatataag aaaagaagac
3001 agtgaaaaaa aaacaatata ggaaagaaaa ataaacatcg attagaaaag aaactgaaat
3061 aaaaaaccgc ctttatgaag ggaatcatat tgtggataag tgtttaggaa atttcatgtg
3121 tgaattttta ttgtctaaaa gggttaacatt ttggaagaag aaagatcaaa aaaaaaagaa
3181 agcaaatttt gtggaacacg attctcttac gggggataac aaacggaatt atgacggtgg
3241 actgtaagga aaaattgaga aagatct

```

//

Revised: July 5, 2002.

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 31 2002 16:00:17

09/673,222 IDS #48



EGCTCAGGATACGACTTCGCTGCTAGATGATCGGATCCCCGGTTCATTATATAGCTCGATCGATC1
TTCTCTATATCCACGCTATGGCTATATACACACACACCCGCGCGATAGCATGACTGATCTA
ECCCACT
CACAGACTCTACGCT

Nucleotide

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	Book
Search	Nucleotide	for	Go	Clear				
Limits	Preview/Index	History	Clipboard	Details				
Display	default	Save	Text	Add to Clipboard	Get Subsequence			

1: AF052191. Strongylocentrotu...[gi:3098602]

Links

LOCUS AF052191 1551 bp mRNA linear INV 05-MAR-2001
DEFINITION Strongylocentrotus purpuratus katanin p60 subunit mRNA, complete cds.
ACCESSION AF052191
VERSION AF052191.1 GI:3098602
KEYWORDS
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 1551)
AUTHORS McNally, F.J. and Vale, R.D.
TITLE Identification of katanin, an ATPase that severs and disassembles stable microtubules
JOURNAL Cell 75 (3), 419-429 (1993)
MEDLINE 94037090
PUBMED 8221885
REFERENCE 2 (bases 1 to 1551)
AUTHORS Hartman, J.J., Mahr, J., McNally, K., Okawa, K., Iwamatsu, A., Thomas, S., Cheesman, S., Heuser, J., Vale, R.D. and McNally, F.J.
TITLE Katanin, a microtubule-severing protein, is a novel AAA ATPase that targets to the centrosome using a WD40-containing subunit
JOURNAL Cell 93 (2), 277-287 (1998)
MEDLINE 98227670
PUBMED 9568719
REFERENCE 3 (bases 1 to 1551)
AUTHORS Hartman, J.J., McNally, F.J. and Vale, R.D.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-1998) Biochemistry and Biophysics, UCSF, 513 Parnassus Ave., San Francisco, CA 94143-0448, USA
FEATURES
source Location/Qualifiers
1..1551
/organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/cell_type="unfertilized egg"
CDS 1..1551
/note="microtubule severing ATPase; severs taxol stabilized microtubules in an ATP-dependent fashion"
/codon_start=1
/product="katanin p60 subunit"
/protein_id="AAC15706.1"
/db_xref="GI:3098603"
/translation="MSVDEICENTKMGREYALLGNYETSLVYYQGV LQQIQKLLTSVH
EPQRKHQWQTI RQELS QEYEHVKNITKTLNGFKSEPAAPNPAPNHRAAPF SHHQHA AK
PAAAE PARDPDVWPPTFPVDHRPSPPYQRAARKDPPRRSEPSKPANRAPGND RGG RGP
SDRRGDARSGGGGRGGARGSDKDKNRGGKSDKDKKAPSGEEDKKFDPAGYDKDLVE
NLERDIVQRNPNVHWADIAGL TEAKRLLEEAVVLP LWPDPYFKGIRRPWKGVLMVGPP
GTGKTMLAKAVATECGTTFFNVSSASLTSKYHGESEKLVRLLFEMARFYAPSTIFIDE
IDSICSKRG TGSEHEASRRVKSELLIQMDGVSGPSAGEESSKMVMVLAATNFPWDIDE
ALRRRLEKRIYIPLPEIDGREQLLRINLKEVPLADDIDLKSIAEKMDGYSGADITNVC

RDASMMAMRRRIQGLRPEEIRHIPKEELNQPSTPADFLLALQKVSKSVGKEDLVKYMA
WMEEFGSV"

BASE COUNT	404 a	410 c	452 g	285 t
ORIGIN				
1	atgagtgtcg	atgaaatctg	cgagaacacc	aagatgggga
61	aactacgaga	catcgctggt	ctactaccaa	ggggtgctcc
121	acatctgtcc	atgaacccca	acgcaagcac	caatggcaaa
181	caagaatacg	agcatgtgaa	gaacatcacc	aagaccctga
241	gctgctccgg	agccagcacc	caaccacagg	gctgccccct
301	gccaagccag	ctgctgccga	gccggcaagg	gaccagatg
361	gtggaccaca	ggccatcccc	tccataccag	agggctgcac
421	agtgagccta	gcaaaccagc	caatcgtgcg	cctggaaacg
481	tcagatcgtc	gtggtgatgc	tcgttcgggt	ggtggtggac
541	gataaagaca	agaatagagg	tgaaaaatca	gataaggata
601	gagggtgacg	agaagaagtt	tgaccagct	ggttatgaca
661	gaaagagaca	ttgtacaaag	gaacccaaat	gttactgagg
721	gaagccaagc	gtctgctaga	agaagccgtg	gttctcccc
781	aagggaatca	gaagaccttg	gaaggggggt	ctgatggtgg
841	accatgctcg	ccaaggcggg	agccaccgaa	tgcgggacga
901	gcttcgctga	cttcgaaata	tcatggagag	tcggaaaagc
961	atggcacgat	tctacgcccc	tagcaccatc	tttatcgatg
1021	aagcgtggaa	cagggctctga	acacgaggct	agcaggaggg
1081	caaattggacg	gtgtgtctgg	acctagcgct	ggtgaggaga
1141	ctcgtgcca	ccaacttccc	ctgggacatc	gacgaagctc
1201	cgtatctaca	ttccgctgcc	agaaatcgac	ggacgtgagc
1261	aaggaagtgc	ctctggctga	tgacattgac	ctcaagagca
1321	tactcaggag	ctgacatcac	caatgtttgc	agagatgcat
1381	cgcatccagg	ggctgcggcc	ggaggagatc	cgccacatcc
1441	cccagcacgc	ccgcagactt	cctgctggcg	ctccagaagg
1501	gaggacctgg	tcaaatacat	ggcgtggatg	gaggagtttg

//

Revised: July 5, 2002.

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Oct 31 2002 15:04:17